

WEST Search History

DATE: Tuesday, October 19, 2004

Hide?	Set Name	Query	Hit Count
	<i>DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ</i>		
<input type="checkbox"/>	L24	(drink or beverage or syrup) and L23	13
<input type="checkbox"/>	L23	(chelate\$6) and L22	52
<input type="checkbox"/>	L22	(l20 or L21) same (zn or zinc)	81
<input type="checkbox"/>	L21	protein near5 (hydrosylate or hdyroy\$5)	58
<input type="checkbox"/>	L20	proteinate	304
<input type="checkbox"/>	L18	protein\$4 near5 hydrozylate	8
<input type="checkbox"/>	L17	(l14 or l15) and (beverage or drink)	0
<input type="checkbox"/>	L16	(l14 or l15) and (beverage or food)	1
<input type="checkbox"/>	L15	us-4172072-\$.did.	2
<input type="checkbox"/>	L14	us-3969540-\$.did.	2
<input type="checkbox"/>	L13	(drink or beverage) same l7	0
<input type="checkbox"/>	L12	L11 not l2	56
<input type="checkbox"/>	L11	(beverage or drink) and L7	57
<input type="checkbox"/>	L10	(beverage or drink) and L8	0
<input type="checkbox"/>	L9	(beverage or drink) same L8	0
<input type="checkbox"/>	L8	(chelate\$9 or cooridan\$7) near10 L7	76
<input type="checkbox"/>	L7	(zinc or zn) near10 (peptid\$8 or oligopeptid\$6 or polypeptid\$8)	2219
<input type="checkbox"/>	L6	l2 not l4	6
<input type="checkbox"/>	L5	L4 not l3	6
<input type="checkbox"/>	L4	food and L2	12
<input type="checkbox"/>	L3	(beverage or drink) and L2	7
<input type="checkbox"/>	L2	(zinc or zn) near5 oligopeptid\$6	18

END OF SEARCH HISTORY

> d his

(FILE 'HOME' ENTERED AT 13:57:27 ON 19 OCT 2004)

FILE 'REGISTRY' ENTERED AT 13:57:41 ON 19 OCT 2004

L1 25 S RDAKGE/SQSP

FILE 'CAPLUS' ENTERED AT 13:59:20 ON 19 OCT 2004

L2 25 S L1
L3 1 S L2 AND HYDROLY?
L4 2 S L2 AND ZINC
L5 1 S 388098-56-4/RN

=> s l2 not l5

L6 24 L2 NOT L5

=> d bib ab hitrn 1-24

L6 ANSWER 1 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2004:770844 CAPLUS

DN 141:237807

TI Sorghum nucleic acids and encoded proteins and their uses improvement of transgenic plants

IN Kovalic, David K.; Zhou, Yihua; Cao, Yongwei

PA USA

SO U.S. Pat. Appl. Publ., 14 pp., Cont.-in-part of U.S. Ser. No. 850,147, abandoned.

CODEN: USXXCO

DT Patent

LA English

FAN.CNT 13

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2004172684	A1	20040902	US 2004-767701	20040129
	US 2004172684	A1	20040902	US 2004-767701	20040129
PRAI	US 2000-684016	A2	20001010		
	US 2001-850147	B2	20010508		
	US 2004-767701	A	20040129		

AB Nucleotide sequences are provided for 31,563 nucleic acids in a cDNA library from sorghum tissue. The open reading frame in each recombinant polynucleotide sequence is identified by a combination of predictive and homol. based methods. Functions of polypeptides encoded by the polynucleotide sequences are detd. using a hierarchical classification tool, termed FunCAT, for Functional Categories Annotation Tool. Functional assignments from five public classification schemes, GO_BP, GO_CC, GO_MF, KEGG, and EC, and one internal Monsanto classification scheme, POI, are also provided. The disclosed recombinant polynucleotides and recombinant polypeptides find use in prodn. of transgenic plants to produce plants having improved properties. [This abstr. record is one of 13 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT 752627-97-7

RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses) (amino acid sequence; sorghum nucleic acids and encoded proteins and their uses improvement of transgenic plants)

L6 ANSWER 2 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2004:209221 CAPLUS

Correction of: 2004:155863

DN 140:212094

Correction of: 140:176338

TI Soybean nucleic acids and encoded proteins associated with transcription in plants and their uses for plant improvement

IN La Rosa, Thomas J.; Zhou, Yihua; Kovalic, David K.; Cao, Yongwei

PA USA
SO U.S. Pat. Appl. Publ., 15 pp., Cont.-in-part of U.S. Ser. No. 985,678, abandoned.
CODEN: USXXCO
DT Patent
LA English

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2004031072 A1		20040212	US 2003-XU424599	20030428
PRAI	US 1999-304517	19990506			
	US 2001-985678	20011105			
	US 2003-424599	20030428			

AB This invention provides 142,842 polynucleotide sequences isolated from a cDNA library generated from Glycine max. The open reading frame in each polynucleotide sequence is identified by a combination of predictive and homol.-based methods. Functions of polypeptides encoded by the polynucleotides sequences are detd. using a hierarchical classification tool, termed FunCAT, for Functional Categories Annotation Tool. Sequences useful for producing transgenic plants having improved biol. properties are identified from their FunCAT annotations. [This abstr. record is one of 72 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT 666531-24-4
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses) (amino acid sequence; soybean nucleic acids and encoded proteins assocd. with transcription in plants and their uses for plant improvement)

L6 ANSWER 3 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2004:155818 CAPLUS
DN 140:194471
TI Nucleic acids and encoded proteins associated with plants and their uses for plant improvement
IN Liu, Jingdong; Zhou, Yihua; Kovalic, David K.; Screen, Steven E.; Tabaska, Jack E.; Cao, Yongwei
PA USA
SO U.S. Pat. Appl. Publ., 15 pp., Cont.-in-part of U.S. Ser. No. 985,678, abandoned.
CODEN: USXXCO
DT Patent
LA English

FAN.CNT 46

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2004034888	A1	20040219	US 2003-425114	20030428
	US 2004034888	A1	20040219	US 2003-425114	20030428
PRAI	US 1999-304517	B1	19990506		
	US 2001-985678	B2	20011105		
	US 2003-425114	A	20030428		

AB This invention provides 36,564 polynucleotide sequences isolated from cDNA libraries generated from various plants, including Zea mays, Glycine max, Arabidopsis thaliana, Lycopersicon esculentum, Oryza sativa, Triticum aestivum, Euglena gracilis, Chlorella vulgaris, Schizochytrium aggregatum, Brassica napus, Gossypium hirsutum, Cucumis sativus, Lilium asiatic, Sorghum bicolor, Chlorella sorokiniana, Cuphea pulcherrima, and Allium porrum. The open reading frame in each polynucleotide sequence is identified by a combination of predictive and homol.-based methods. Functions of polypeptides encoded by the polynucleotides sequences are detd. using a hierarchical classification tool, termed FunCAT, for Functional Categories Annotation Tool. Sequences useful for producing transgenic plants having improved biol. properties are identified from their FunCAT annotations. [This abstr. record is one of 19 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT 662212-44-4

RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses) (amino acid sequence; nucleic acids and encoded proteins assocd. with plants and their uses for plant improvement)

L6 ANSWER 4 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2004:11575 CAPLUS

DN 140:158553

TI Expression of microbial proteins in plants for production of plants with improved properties

IN Cao, Yongwei; Hinkle, Gregory J.; Slater, Steven C.; Chen, Xianfeng; Goldman, Barry S.

PA USA

SO U.S. Pat. Appl. Publ., 122 pp.

CODEN: USXXCO

DT Patent

LA English

FAN.CNT 12

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2003233675	A1	20031218	US 2003-369493	20030220
PRAI	US 2002-360039P	P	20020221		

AB Recombinant constructs and methods useful for improvement of plants are provided. In particular, recombinant constructs comprising promoters functional in plant cells positioned for expression of polynucleotides encoding polypeptides from microbial sources are provided. The disclosed constructs and methods find use in prodn. of transgenic plants to provide plants, particularly crop plants, having improved properties. [This abstr. record is one of twelve records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints].

IT 654729-89-2P

RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)

(amino acid sequence; expression of microbial proteins in plants for prodn. of plants with improved properties)

L6 ANSWER 5 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2003:991248 CAPLUS

DN 140:37065

TI Expression of microbial proteins in plants for production of plants with improved properties

IN Cao, Yongwei; Hinkle, Gregory J.; Slater, Steven C.; Chen, Xianfeng; Goldman, Barry S.

PA USA

SO U.S. Pat. Appl. Publ., 122 pp.

CODEN: USXXCO

DT Patent

LA English

FAN.CNT 12

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2003233675	A1	20031218	US 2003-369493	20030220
PRAI	US 2002-360039P	P	20020221		

AB Recombinant constructs and methods useful for improvement of plants are provided. In particular, recombinant constructs comprising promoters functional in plant cells positioned for expression of polynucleotides encoding polypeptides from microbial sources are provided. The disclosed constructs and methods find use in prodn. of transgenic plants to provide plants, particularly crop plants, having improved properties. [This abstr. record is one of twelve records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints].

IT 636636-60-7P

RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; expression of microbial proteins in plants for prodn. of plants with improved properties)

L6 ANSWER 6 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2003:816570 CAPLUS

DN 139:287121

TI Complete genome sequence and analysis of *Wolinella succinogenes*

AU Baar, Claudia; Eppinger, Mark; Raddatz, Guenter; Simon, Joerg; Lanz, Christa; Klimmek, Oliver; Nandakumar, Ramkumar; Gross, Roland; Rosinus, Andrea; Keller, Heike; Jagtap, Pratik; Linke, Burkhard; Meyer, Folker; Lederer, Hermann; Schuster, Stephan C.

CS Max Planck Institute for Developmental Biology, Tuebingen, 72076, Germany

SO Proceedings of the National Academy of Sciences of the United States of America (2003), 100(20), 11690-11695

CODEN: PNASA6; ISSN: 0027-8424

PB National Academy of Sciences

DT Journal

LA English

AB To understand the origin and emergence of pathogenic bacteria, knowledge of the genetic inventory from their nonpathogenic relatives is a prerequisite. Therefore, the 2.11-megabase genome sequence of *Wolinella succinogenes*, which is closely related to the pathogenic bacteria *Helicobacter pylori* and *Campylobacter jejuni*, was detd. Despite being considered nonpathogenic to its bovine host, *W. succinogenes* holds an extensive repertoire of genes homologous to known bacterial virulence factors. Many of these genes have been acquired by lateral gene transfer, because part of the virulence plasmid pVir and an N-linked glycosylation gene cluster were found to be syntenic between *C. jejuni* and genomic islands of *W. succinogenes*. In contrast to other host-adapted bacteria, *W. succinogenes* does harbor the highest d. of bacterial sensor kinases found in any bacterial genome to date, together with an elaborate signaling circuitry of the GGDEF family of proteins. Because the anal. of the *W. succinogenes* genome also revealed genes related to soil- and plant-assocd. bacteria such as the nif genes, *W. succinogenes* may represent a member of the epsilon proteobacteria with a life cycle outside its host. The genome sequence is deposited in GenBank/EMBL/DDBJ under accession no. BX571656 and in the RefSeq Genome Database under accession no. NC_005090 and is also available at www.wolinella.mpg.de.

IT 581750-19-8

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; complete genome sequence and anal. of *Wolinella succinogenes*)

RE.CNT 66 THERE ARE 66 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 7 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2003:539800 CAPLUS

DN 139:64475

TI Abiotic stress responsive polynucleotides and polypeptides from plants and methods of altering the stress responsiveness of a plant

IN Kreps, Joel; Briggs, Steven P.; Cooper, Bret; Glazebrook, Jane; Goff, Stephen A.; Katagiri, Fumiyaki; Moughamer, Todd; Provart, Nicholas; Ricke, Darrell; Zhu, Tong

PA Syngenta Participations AG, Switz.

SO PCT Int. Appl., 177 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 9

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003008540	A2	20030130	WO 2002-XA19668	20020621

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

WO 2003008540 A2 20030130 WO 2002-US19668 20020621

WO 2003008540 A3 20031204

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 2003135888 A1 20030717 US 2002-259165 20020926

US 2004010815 A1 20040115 US 2002-259194 20020926

US 2004016025 A1 20040122 US 2002-260238 20020926

PRAI US 2001-300112P P 20010622

US 2001-314662P P 20010824

US 2001-325277P P 20010926

US 2001-332132P P 20011121

WO 2002-US19668 A 20020621

US 2001-325448P P 20010926

US 2002-368327P P 20020327

US 2002-370620P P 20020404

US 2002-370743P P 20020404

AB Abiotic stress responsive polynucleotides and polypeptides are disclosed. Also disclosed are vectors, expression cassettes, host cells, and plants contg. such polynucleotides. Also provided are methods for using such polynucleotides and polypeptides, for example, to alter the responsiveness of a plant to abiotic stress. Rice (*Oryza sativa japonica*) cDNA library was constructed and sequenced, and used in GeneChip std. protocol for expression profiling of stress-regulated genes. Based on the profiles, clusters of nucleic sequences that were altered at least two-fold in response to the stress condition were identified. Identification of abiotic stress responsive genes using yeast two hybrid system was also demonstrated. Rice orthologs of Arabidopsis abiotic stress genes were identified by reverse genetics. Transgenic rice expressing "abiotic stress candidate gene" was produced. The present invention claimed abiotic stress responsive cDNAs (SEQ IDs 1-4131, 8263-8353, 8445-8829 and 17505-17506) and proteins (SEQ IDs 4132-8262, 8354-8444, and 8830-9214), but the Sequence Listing was not made available on publication of the patent application.

IT 549577-49-3

RL: PRP (Properties)
(unclaimed protein sequence; abiotic stress responsive polynucleotides and polypeptides from plants and methods of altering the stress responsiveness of a plant)

L6 ANSWER 8 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2003:326641 CAPLUS

DN 138:298932

TI Nucleic acid and amino acid sequences relating to *Pseudomonas aeruginosa* for diagnostics and therapeutics

IN Rubenfield, Marc J.; Nolling, Jork; Deloughery, Craig; Bush, David

PA Genome Therapeutics Corporation, USA

SO U.S., 455 pp.

CODEN: USXXAM

DT Patent
LA English
FAN.CNT 8

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 6551795	B1	20030422	US 1999-252991	19990218
	US 6551795	B1	20030422	US 1999-252991	19990218
PRAI	US 1998-74788P	P	19980218		
	US 1998-94190P	P	19980727		
	US 1999-252991	A	19990218		

AB The invention provides 16,571 isolated polypeptide and their encoding nucleic acid sequences derived from *Pseudomonas aeruginosa* strain 19804 (ATCC #20204) that are useful in diagnosis and therapy of pathol. conditions, antibodies against the polypeptides, and methods for the prodn. of the polypeptides. The invention also provides methods for the detection, prevention and treatment of pathol. conditions resulting from bacterial infection. [This abstr. record is one of eight records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints].

IT 508416-10-2

RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (amino acid sequence; nucleic acid and amino acid sequences relating to *Pseudomonas aeruginosa* for diagnostics and therapeutics)

L6 ANSWER 9 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2003:48581 CAPLUS

DN 138:363478

TI Complete genome sequence and comparative analysis of the metabolically versatile *Pseudomonas putida* KT2440

AU Nelson, K. E.; Weinel, C.; Paulsen, I. T.; Dodson, R. J.; Hilbert, H.; Martins dos Santos, V. A. P.; Fouts, D. E.; Gill, S. R.; Pop, M.; Holmes, M.; Brinkac, L.; Beanan, M.; DeBoy, R. T.; Daugherty, S.; Kolonay, J.; Madupu, R.; Nelson, W.; White, O.; Peterson, J.; Khouri, H.; Hance, I.; Lee, P. Chris; Holtzapple, E.; Scanlan, D.; Tran, K.; Moazzez, A.; Utterback, T.; Rizzo, M.; Lee, K.; Kosack, D.; Moestl, D.; Wedler, H.; Lauber, J.; Stjepandic, D.; Hoheisel, J.; Straetz, M.; Heim, S.; Kiewitz, C.; Eisen, J.; Timmis, K. N.; Dusterhoft, A.; Tummler, B.; Fraser, C. M.

CS The Institute for Genomic Research (TIGR), Rockville, MD, 20850, USA

SO Environmental Microbiology (2002), 4(12), 799-808

CODEN: ENMIFM; ISSN: 1462-2912

PB Blackwell Science Ltd.

DT Journal

LA English

AB *Pseudomonas putida* is a metabolically versatile saprophytic soil bacterium that has been certified as a biosafety host for the cloning of foreign genes. The bacterium also has considerable potential for biotechnol. applications. Sequence anal. of the 6.18 Mb genome of strain KT2440 reveals diverse transport and metabolic systems. A total of 5420 open reading frames with an av. length of 998 bp were identified, with putative role assignments made for 3571 ORFs and another 600 ORFs being unique to *P. putida*. Although there is a high level of genome conservation with the pathogenic *Pseudomonas aeruginosa* (85% of the predicted coding regions are shared), key virulence factors including exotoxin A and type III secretion systems are absent. Anal. of the genome gives insight into the non-pathogenic nature of *P. putida* and points to potential new applications in agriculture, biocatalysis, bioremediation and bioplastic prodn. The genome sequence is deposited in GenBank/EMBL/DBJ under accession no. AE015451 and in the RefSeq database under accession no. NC_002947.

IT 500091-11-2

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; complete genome sequence and comparative anal. of the metabolically versatile *Pseudomonas putida* KT2440)

RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 10 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 2002:795291 CAPLUS
 DN 137:273863
 TI The *Brucella suis* genome reveals fundamental similarities between animal and plant pathogens and symbionts
 AU Paulsen, Ian T.; Seshadri, Rekha; Nelson, Karen E.; Eisen, Jonathan A.; Heidelberg, John F.; Read, Timothy D.; Dodson, Robert J.; Umayam, Lowell; Brinkac, Lauren M.; Beanan, Maureen J.; Daugherty, Sean C.; Deboy, Robert T.; Durkin, A. Scott; Kolonay, James F.; Madupu, Ramana; Nelson, William C.; Ayodeji, Bola; Kraul, Margaret; Shetty, Jyoti; Malek, Joel; Van Aken, Susan E.; Riedmuller, Steven; Tettelin, Herve; Gill, Steven R.; White, Owen; Salzberg, Steven L.; Hoover, David L.; Lindler, Luther E.; Halling, Shirley M.; Boyle, Stephen M.; Fraser, Claire M.
 CS The Institute for Genomic Research, Rockville, MD, 20850, USA
 SO Proceedings of the National Academy of Sciences of the United States of America (2002), 99(20), 13148-13153
 CODEN: PNASA6; ISSN: 0027-8424
 PB National Academy of Sciences
 DT Journal
 LA English
 AB The 3.31-Mb genome sequence of the intracellular pathogen and potential bioterrorism agent, *Brucella suis*, was detd. Comparison of *B. suis* with *Brucella melitensis* has defined a finite set of differences that could be responsible for the differences in virulence and host preference between these organisms, and indicates that phage have played a significant role in their divergence. Anal. of the *B. suis* genome reveals transport and metabolic capabilities akin to soil/plant-assocd. bacteria. Extensive gene synteny between *B. suis* chromosome I and the genome of the plant symbiont *Mesorhizobium loti* emphasizes the similarity between this animal pathogen and plant pathogens and symbionts. A limited repertoire of genes homologous to known bacterial virulence factors were identified. The sequences have been deposited in the GenBank/EMBL/DDBJ database under accession nos. AE014291 (chromosome I) and AE014292 (chromosome II), and in the RefSeq database under accession nos. NC_004310 and NC_004311.
 IT 464370-57-8
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (amino acid sequence; complete genome sequence of *Brucella suis* reveals fundamental similarities between animal and plant pathogens and symbionts)
 RE.CNT 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 11 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 2002:781493 CAPLUS
 DN 138:1097
 TI Essential genes in microorganisms and their use as targets for antisense inhibition of proliferation and antibiotic screening
 IN Wang, Liangus; Zamudio, Carlos; Malone, Cheryl; Haselbeck, Robert; Ohlsen, Kari L.; Zyskind, Judith W.; Wall, Daniel; Trawick, John D.; Carr, Grant J.; Yamamoto, Robert; Forsyth, R. Allyn; Xu, H. Howard
 PA Elitra Pharmaceuticals, Inc., USA
 SO PCT Int. Appl., 1766 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 FAN.CNT 22

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002077183	A2	20021003	WO 2002-XP9107	20020321
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DE, DK, DK, DM, DZ, EC, EE, EE, ES, FI, FI, GB, GD, GE, GH, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO,				

NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG

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US 2002061569 A1 20020523 US 2001-815242 20010321

WO 2002077183 A2 20021003 WO 2002-US9107 20020321

W: AE, AG, AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, CZ, DE, DE, DK, DK, DM, DZ, EC, EE, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRAI US 2001-815242 A 20010321

US 2001-948993 A 20010906

US 2001-342923P P 20011025

US 2002-72851 A 20020208

US 2002-362699P P 20020306

WO 2002-US9107 A 20020321

US 2000-191078P P 20000321

US 2000-206848P P 20000523

US 2000-207727P P 20000526

US 2000-242578P P 20001023

US 2000-253625P P 20001127

US 2000-257931P P 20001222

US 2001-269308P P 20010216

AB The sequences of antisense nucleic acids which inhibit the proliferation of prokaryotes are disclosed. Thus, 6213 nucleic acid fragments are identified for which expression inhibits proliferation or is required for proliferation in *Enterococcus faecalis*, *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, and *Staphylococcus aureus*. Cell-based assays which employ the antisense nucleic acids to identify and develop antibiotics are also disclosed. The antisense nucleic acids can also be used to identify proteins required for proliferation, express these proteins or portions thereof, obtain antibodies capable of specifically binding to the expressed proteins, and to use those expressed proteins as a screen to isolate candidate mols. for rational drug discovery programs. The nucleic acids can also be used to screen for homologous nucleic acids that are required for proliferation in cells other than *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa*. The invention provides 38,184 such proliferation-required gene sequences (plus their encoded protein sequences). The nucleic acids of the present invention can also be used in various assay systems to screen for proliferation required genes in other organisms. [This abstr. record is one of twenty records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT 477133-65-6

RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(amino acid sequence; essential genes in microorganisms and their use as targets for antisense inhibition of proliferation and antibiotic screening)

L6 ANSWER 12 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2002:655935 CAPLUS

DN 137:180584

TI Complete genome structure of *Mesorhizobium loti* strain MAFF303099

AU Kaneko, T.; Nakamura, Y.; Sato, S.; Asamizu, E.; Kato, T.; Tabata, S.

CS Kazusa DNA Research Institute, Chiba, 292-0812, Japan

SO Nitrogen Fixation: Global Perspectives, Proceedings of the International

Congress on Nitrogen Fixation, 13th, Hamilton, ON, Canada, July 2-7, 2001
(2002), Meeting Date 2001, 82-85. Editor(s): Finan, Turlough M.
Publisher: CABI Publishing, Wallingford, UK.
CODEN: 69CVYW; ISBN: 0-85199-591-8

DT Conference

LA English

AB The complete genome of *Mesorhizobium loti* strain MAFF303099 has been sequenced by assembly of 90,706 genome survey sequences during shotgun sequencing. The length of the genome was 7,596,297 bp long, which consists of three circular mols., a chromosome 7,036,071 bp and two plasmids, designed as pMLa and pMLb, of 351,911 bp and 208,315 bp, resp. The total no. of potential protein-coding genes assigned to the chromosome was 6752 and the plasmids pMLa and pMLb had the capacity of coding for 320 and 209 proteins. Functional assignment of the protein-coding genes and notable features of the genes are discussed. The sequences are deposited in GenBank under Accession Nos. BA000012 (chromosome), BA000013 (pMLa), and AP003017 (pMLb).

IT 448344-49-8

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; complete genome structure of *Mesorhizobium loti* strain MAFF303099)

L6 ANSWER 13 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2002:434398 CAPLUS

DN 136:396771

TI Complete genome sequence of the model actinomycete *Streptomyces coelicolor* A3(2)

AU Bentley, S. D.; Chater, K. F.; Cerdano-Tarraga, A.-M.; Challis, G. L.; Thomson, N. R.; James, K. D.; Harris, D. E.; Quail, M. A.; Kieser, H.; Harper, D.; Bateman, A.; Brown, S.; Chandra, G.; Chen, C. W.; Collins, M.; Cronin, A.; Fraser, A.; Goble, A.; Hidalgo, J.; Hornsby, T.; Howarth, S.; Huang, C.-H.; Kieser, T.; Larke, L.; Murphy, L.; Oliver, K.; O'Neil, S.; Rabinowitsch, E.; Rajandream, M.-A.; Rutherford, K.; Rutter, S.; Seeger, K.; Saunders, D.; Sharp, S.; Squares, R.; Squares, S.; Taylor, K.; Warren, T.; Wietzorrek, A.; Woodward, J.; Barrell, B. G.; Parkhill, J.; Hopwood, D. A.

CS Wellcome Trust Genome Campus, The Wellcome Trust Sanger Institute, Hinxton, Cambridge, CB10 1SA, UK

SO Nature (London, United Kingdom) (2002), 417(6885), 141-147

CODEN: NATUAS; ISSN: 0028-0836

PB Nature Publishing Group

DT Journal

LA English

AB *Streptomyces coelicolor* is a representative of the group of soil-dwelling, filamentous bacteria responsible for producing most natural antibiotics used in human and veterinary medicine. The 8,667,507 base pair linear chromosome of this organism, contg. the largest no. of genes so far discovered in a bacterium, is reported. The 7825 predicted genes include more than 20 clusters coding for known or predicted secondary metabolites. The genome contains an unprecedented proportion of regulatory genes, predominantly those likely to be involved in responses to external stimuli and stresses, and many duplicated gene sets that may represent 'tissue-specific' isoforms operating in different phases of colonial development, a unique situation for a bacterium. An ancient synteny was revealed between the central 'core' of the chromosome and the whole chromosome of pathogens *Mycobacterium tuberculosis* and *Corynebacterium diphtheriae*. The genome sequence will greatly increase our understanding of microbial life in the soil as well as aiding the generation of new drug candidates by genetic engineering. The complete sequence is deposited in GenBank/EMBL under accession no. AL645882. [This abstr. record is one of two records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT 430499-86-8

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL

(Biological study)
(amino acid sequence; complete genome sequence of the model
actinomycete *Streptomyces coelicolor* A3(2))

L6 ANSWER 14 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:256427 CAPLUS
DN 136:291001
TI Bacterial genes for enzymes of isoprenoid biosynthesis and the engineering
of isoprenoid metabolism
IN Gokarn, Ravi; Jessen, Holly; Zidwick, Mary Jo
PA Cargill Incorporated, USA
SO PCT Int. Appl., 246 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002026933	A2	20020404	WO 2001-US30328	20010928
	WO 2002026933	C2	20030814		
	WO 2002026933	A3	20031106		
	W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
	RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
	EP 1383864	A2	20040128	EP 2001-977223	20010928
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR			
	US 2003219798	A1	20031127	US 2003-381779	20030328
PRAI	US 2000-236580P	P	20000929		
	WO 2001-US30328	W	20010928		

AB The invention provides methods and materials related to the prodn. of isoprenoids. Specifically, the invention provides cloned genes for enzymes of polyisoprenoid biosynthesis and the enzymes and cells expressing the cloned genes for use in the manuf. of isoprenoids such as enzyme Q10. Genes for the enzymes were cloned from *Sphingomonas trueperi* and *Rhodobacter sphaeroides* by PCR using primers derived from known genes for the enzymes. Construction of expression vectors and expression hosts is described. Specifically, hosts in which genes for enzymes that would draw isopentenyl pyrophosphate away from coenzyme Q10 biosynthesis are inactivated are described. Inactivation of any one of these genes increases the yield of coenzyme Q10.

IT 408543-21-5
RL: PRP (Properties)
(unclaimed sequence; bacterial genes for enzymes of isoprenoid biosynthesis and the engineering of isoprenoid metab.)

L6 ANSWER 15 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:52480 CAPLUS
DN 136:113581
TI The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
AU DeVecchio, Vito G.; Kapatal, Vinayak; Redkar, Rajendra J.; Patra, Guy; Mujer, Cesar; Los, Tamara; Ivanova, Natalia; Anderson, Iain; Bhattacharyya, Anamitra; Lykidis, Athanasios; Reznik, Gary; Jablonski, Lynn; Larsen, Niels; D'Souza, Mark; Bernal, Axel; Mazur, Mikhail; Goltsman, Eugene; Selkov, Eugene; Elzer, Philip H.; Hagius, Sue; O'Callaghan, David; Letesson, Jean-Jacques; Haselkorn, Robert; Kyrpides, Nikos; Overbeek, Ross
CS Institute of Molecular Biology and Medicine, University of Scranton, Scranton, PA, 18510, USA

SO Proceedings of the National Academy of Sciences of the United States of America (2002), 99(1), 443-448
CODEN: PNASA6; ISSN: 0027-8424

PB National Academy of Sciences
DT Journal
LA English

AB *Brucella melitensis* is a facultative intracellular bacterial pathogen that causes abortion in goats and sheep and Malta fever in humans. The genome of *B. melitensis* strain 16M was sequenced and found to contain 3,294,935 bp distributed over two circular chromosomes of 2,117,144 bp and 1,177,787 bp encoding 3,197 ORFs. By using the bioinformatics suite ERGO, 2487 (78%) ORFs were assigned functions. The origins of replication of the two chromosomes are similar to those of other α -proteobacteria. Housekeeping genes, including those involved in DNA replication, transcription, translation, core metab., and cell wall biosynthesis, are distributed on both chromosomes. Type I, II, and III secretion systems are absent, but genes encoding sec-dependent, sec-independent, and flagella-specific type III, type IV, and type V secretion systems as well as adhesins, invasins, and hemolysins were identified. Several features of the *B. melitensis* genome are similar to those of the symbiotic *Sinorhizobium meliloti*.

IT 389684-36-0
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence of the facultative intracellular pathogen *Brucella melitensis*)

RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 16 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:763196 CAPLUS
DN 135:328142

TI Lactococcus lactis genome and polypeptides and their uses
IN Bolotine, Alexandre; Sorokine, Alexei; Renault, Pierre; Ehrlich, Stanislaw Dusko
PA Institut National de la Recherche Agronomique, Fr.
SO PCT Int. Appl., 218 pp.
CODEN: PIXXD2
DT Patent
LA French

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001077334	A2	20011018	WO 2001-FR1103	20010411
	WO 2001077334	A3	20020228		
	WO 2001077334	C2	20030123		
	W:		AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM		
	RW:		GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG		
	FR 2807446	A1	20011012	FR 2000-4630	20000411
PRAI	FR 2000-4630	A	20000411		

AB The invention concerns the nucleotide sequence of the genome sequence of *Lactococcus lactis* IL1403. The invention also concerns 2322 polypeptides of said organism, in particular cell envelope polypeptides, polypeptides involved in different metab. cycles, resistance to phages or stress, or still secreted polypeptides. The invention further concerns the use of said sequences, and different tools for identifying *L. lactis* or assocd. species. Finally, the invention concerns *L. lactis* strains modified so as to increase their industrial properties.

IT 341585-51-1

RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)

(amino acid sequence; *Lactococcus lactis* genome and polypeptides and their uses)

L6 ANSWER 17 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:634531 CAPLUS
DN 136:258038
TI Analysis of the chromosome sequence of the legume symbiont *Sinorhizobium meliloti* strain 1021
AU Capela, Delphine; Barloy-Hubler, Frederique; Gouzy, Jerome; Bothe, Gordana; Ampe, Frederic; Batut, Jacques; Boistard, Pierre; Becker, Anke; Boutry, Marc; Cadieu, Edouard; Dreano, Stephane; Gloux, Stephanie; Godrie, Therese; Goffeau, Andre; Kahn, Daniel; Kiss, Erno; Lelaure, Valerie; Masuy, David; Pohl, Thomas; Portetelle, Daniel; Puhler, Alfred; Purnelle, Benedicte; Ramsperger, Ulf; Renard, Clotilde; Thebault, Patricia; Vandebol, Micheline; Weidner, Stefan; Galibert, Francis
CS Laboratoire de Biologie Moleculaire des Relations Plantes-Microorganismes, Unite Mixte de Recherche (UMR) 215 Centre National de la Recherche Scientifique (CNRS), Institut National de la Recherche Agronomique, Chemin, Tolosan, F-31326, Fr.
SO Proceedings of the National Academy of Sciences of the United States of America (2001), 98(17), 9877-9882
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB *Sinorhizobium meliloti* is an α -proteobacterium that forms agronomically important N₂-fixing root nodules in legumes. We report here the complete sequence of the largest constituent of its genome, a 62.7% GC-rich 3654,135-bp circular chromosome. Annotation allowed assignment of a function to 59% of the 3341 predicted protein-coding ORFs, the rest exhibiting partial, weak, or no similarity with any known sequence. Unexpectedly, the level of reiteration within this replicon is low, with only two genes duplicated with more than 90% nucleotide sequence identity, transposon elements accounting for 2.2% of the sequence, and a few hundred short repeated palindromic motifs (RIME1, RIME2, and C) widespread over the chromosome. Three regions with a significantly lower GC content are most likely of external origin. Detailed annotation revealed that this replicon contains all housekeeping genes except two essential genes that are located on pSymB. Amino acid/peptide transport and degradn. and sugar metab. appear as two major features of the *S. meliloti* chromosome. The presence in this replicon of a large no. of nucleotide cyclases with a peculiar structure, as well as of genes homologous to virulence determinants of animal and plant pathogens, opens perspectives in the study of this bacterium both as a free-living soil microorganism and as a plant symbiont.
IT 353890-17-2
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; anal. of chromosome sequence of legume symbiont *Sinorhizobium meliloti* strain 1021)
RE.CNT 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 18 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:566348 CAPLUS
DN 135:176294
TI The composite genome of the legume symbiont *Sinorhizobium meliloti*
AU Galibert, Francis; Finan, Turlough M.; Long, Sharon R.; Puhler, Alfred; Abola, Pia; Ampe, Frederic; Barloy-Hubler, Fredherique; Barnett, Melanie J.; Becker, Anke; Boistard, Pierre; Bothe, Gordana; Boutry, Marc; Bowser, Leah; Buhrmester, Jens; Cadieu, Edouard; Capela, Delphine; Chain, Patrick; Cowie, Alison; Davis, Ronald W.; Dreano, Stiphane; Federspiel, Nancy A.;

Fisher, Robert F.; Gloux, Stephanie; Godrie, Therese; Goffeau, Andre;
Golding, Brian; Gouzy, Jerome; Gurjal, Mani; Hernandez-Lucas, Ismael;
Hong, Andrea; Huizar, Lucas; Hyman, Richard W.; Jones, Ted; Kahn, Daniel;
Kahn, Michael L.; Kalman, Sue; Keating, David H.; Kiss, Erno; Komp,
Caridad; LeLaure, Valerie; Masuy, David; Palm, Curtis; Peck, Melicent C.;
Pohl, Thomas M.; Portetelle, Daniel; Purnelle, Benedicte; Ramsperger, Uwe;
Surzycki, Raymond; Thebault, Patricia; Vandenberg, Micheline; Vorholter,
Frank-J.; Weidner, Stefan; Wells, Derek H.; Wong, Kim; Yeh, Kuo-Chen;
Batut, Jacques

CS Laboratoire de Genetique et Developpement, Faculte de Medecine,
UMR6061-CNRS, Rennes, F-35043, Fr.

SO Science (Washington, DC, United States) (2001), 293(5530), 668-672
CODEN: SCIEAS; ISSN: 0036-8075

PB American Association for the Advancement of Science

DT Journal

LA English

AB The scarcity of usable nitrogen frequently limits plant growth. A tight
metabolic assocn. with rhizobial bacteria allows legumes to obtain
nitrogen compds. by bacterial redn. of dinitrogen (N₂) to ammonium (NH₄⁺).
The annotated DNA sequence of the α -proteobacterium *Sinorhizobium*
meliloti, the symbiont of alfalfa, is presented. The tripartite
6.7-megabase (Mb) genome comprises a 3.65-Mb chromosome, and 1.35-Mb pSymA
and 1.68-Mb pSymB megaplasms. Genome sequence anal. indicates that all
three elements contribute, in varying degrees, to symbiosis and reveals
how this genome may have emerged during evolution. The genome sequence
will be useful in understanding the dynamics of interkingdom assocns. and
of life in soil environments. The chromosome, pSymA, and pSymB sequences
are available in GenBank Accession Nos. AE007195-AE007315,
AL591782-AL591793, and AL603642-AL603647, resp.

IT 353890-17-2
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(amino acid sequence; composite genome of the legume symbiont
Sinorhizobium meliloti)

RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 19 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2001:401771 CAPLUS

DN 138:33912

TI Complete genome sequence of *Caulobacter crescentus*. [Erratum to document
cited in CA134:276385]

AU Nierman, William C.; Feldblyum, Tamara V.; Laub, Michael T.; Paulsen, Ian
T.; Nelson, Karen E.; Eisen, Jonathan A.; Heidelberg, John F.; Alley, M.
R. K.; Ohta, Noriko; Maddock, Janine R.; Potocka, Isabel; Nelson, William
C.; Newton, Austin; Stephens, Craig; Phadke, Nikhil D.; Ely, Bert; DeBoy,
Robert T.; Dodson, Robert J.; Durkin, A. Scott; Gwinn, Michelle L.; Haft,
Daniel H.; Kolonay, James F.; Smit, John; Craven, M. B.; Lhoury, Hoda;
Shetty, Jyoti; Berry, Kristi; Utterback, Teresa; Tran, Kevin; Wolf, Alex;
Vamathevan, Jessica; Ermolaeva, Maria; White, Owen; Salzberg, Steven L.;
Venter, J. Craig; Shapiro, Lucy; Fraser, Claire M.

CS The Institute for Genomic Research, Rockville, MD, 20850, USA

SO Proceedings of the National Academy of Sciences of the United States of
America (2001), 98(11), 6533
CODEN: PNASA6; ISSN: 0027-8424

PB National Academy of Sciences

DT Journal

LA English

AB Jonathan Eisen should be listed as Jonathan A. Eisen.

IT 332980-00-4
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(amino acid sequence; complete genome sequence of *Caulobacter*
crescentus (Erratum))

L6 ANSWER 20 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2001:361583 CAPLUS
 DN 135:71980
 TI The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ssp. *lactis* IL1403
 AU Bolotin, Alexander; Wincker, Patrick; Mauger, Stephane; Jaillon, Olivier; Malarme, Karine; Weissenbach, Jean; Ehrlich, S. Dusko; Sorokin, Alexei
 CS Genetique Microbienne, Institut National de la Recherche Agronomique, Jouy en Josas, 78352, Fr.
 SO Genome Research (2001), 11(5), 731-753
 CODEN: GEREFS; ISSN: 1088-9051
 PB Cold Spring Harbor Laboratory Press
 DT Journal
 LA English
 AB *Lactococcus lactis* is a nonpathogenic AT-rich gram-pos. bacterium closely related to the genus *Streptococcus* and is the most commonly used cheese starter. It is also the best-characterized lactic acid bacterium. The genome of the lab. strain IL1403 was sequenced, using a novel two-step strategy that comprises diagnostic sequencing of the entire genome and a shotgun polishing step. The genome contains 2,365,589 base pairs and encodes 2310 proteins, including 293 protein-coding genes belonging to 6 prophages and 43 insertion sequence (IS) elements. Nonrandom distribution of IS elements indicates that the chromosome of the sequenced strain may be a product of recent recombination between two closely related genomes. A complete set of late competence genes is present, indicating the ability of *L. lactis* to undergo DNA transformation. Genomic sequence revealed new possibilities for fermn. pathways and for aerobic respiration. It also indicated a horizontal transfer of genetic information from *Lactococcus* to gram-neg. enteric bacteria of *Salmonella*-*Escherichia* group.
 IT 341585-51-1
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (amino acid sequence; complete genome sequence of *Lactococcus lactis* ssp. *lactis* IL1403)
 RE.CNT 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 21 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 2001:266262 CAPLUS
 DN 134:276385
 TI Complete genome sequence of *Caulobacter crescentus*
 AU Nierman, William C.; Feldblyum, Tamara V.; Laub, Michael T.; Paulsen, Ian T.; Nelson, Karen E.; Eisen, Jonathan; Heidelberg, John F.; Alley, M. R. K.; Ohta, Noriko; Maddock, Janine R.; Potocka, Isabel; Nelson, William C.; Newton, Austin; Stephens, Craig; Phadke, Nikhil D.; Ely, Bert; DeBoy, Robert T.; Dodson, Robert J.; Durkin, A. Scott; Gwinn, Michelle L.; Haft, Daniel H.; Kolonay, James F.; Smit, John; Craven, M. B.; Khouri, Hoda; Shetty, Jyoti; Berry, Kristi; Utterback, Teresa; Tran, Kevin; Wolf, Alex; Vamathevan, Jessica; Ermolaeva, Maria; White, Owen; Salzberg, Steven L.; Venter, J. Craig; Shapiro, Lucy; Fraser, Claire M.
 CS The Institute for Genomic Research, Rockville, MD, 20850, USA
 SO Proceedings of the National Academy of Sciences of the United States of America (2001), 98(7), 4136-4141
 CODEN: PNASA6; ISSN: 0027-8424
 PB National Academy of Sciences
 DT Journal
 LA English
 AB The complete genome sequence of *Caulobacter crescentus* was detd. to be 4,016,942 base pairs in a single circular chromosome encoding 3767 genes. This organism, which grows in a dil. aquatic environment, coordinates the cell division cycle and multiple cell differentiation events. With the annotated genome sequence, a full description of the genetic network that controls bacterial differentiation, cell growth, and cell cycle progression is within reach. Two-component signal transduction proteins are known to play a significant role in cell cycle progression. Genome anal. revealed that the *C. crescentus* genome encodes a significantly higher no. of these signaling proteins (105) than any bacterial genome

sequenced thus far. Another regulatory mechanism involved in cell cycle progression is DNA methylation. The occurrence of the recognition sequence for an essential DNA methylating enzyme that is required for cell cycle regulation is severely limited and shows a bias to intergenic regions. The genome contains multiple clusters of genes encoding proteins essential for survival in a nutrient poor habitat. Included are those involved in chemotaxis, outer membrane channel function, degrdn. of arom. ring compds., and the breakdown of plant-derived carbon sources, in addn. to many extracytoplasmic function sigma factors, providing the organism with the ability to respond to a wide range of environmental fluctuations. *C. crescentus* is, to our knowledge, the first free-living .alpha.-class proteobacterium to be sequenced and will serve as a foundation for exploring the biol. of this group of bacteria, which includes the obligate endosymbiont and human pathogen *Rickettsia prowazekii*, the plant pathogen *Agrobacterium tumefaciens*, and the bovine and human pathogen *Brucella abortus*.

IT 332980-00-4

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of *Caulobacter crescentus*)

RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 22 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2000:636908 CAPLUS

DN 133:262066

TI Complete genome sequence of *Pseudomonas aeruginosa* PA01

AU Stover, C. K.; Pham, X. Q.; Erwin, A. L.; Mizoguchi, S. D.; Warrenner, P.; Hickey, M. J.; Brinkman, F. S. L.; Hufnagle, W. O.; Kowalik, J.; Lagrou, M.; Garber, R. L.; Goltry, L.; Tolentino, E.; Westbrook-Wadman, S.; Yuan, Y.; Brody, L. L.; Coulter, S. N.; Folger, K. R.; Kas, A.; Larbig, K.; Lim, R.; Smith, K.; Spencer, D.; Wong, G. K.-S.; Wu, Z.; Paulsen, I. T.; Reizer, J.; Saier, M. H.; Hancock, R. E. W.; Lory, S.; Olson, M. V.

CS PathoGenesis Corporation, Seattle, WA, 98119, USA

SO Nature (London) (2000), 406(6799), 959-964

CODEN: NATUAS; ISSN: 0028-0836

PB Nature Publishing Group

DT Journal

LA English

AB *Pseudomonas aeruginosa* is a ubiquitous environmental bacterium that is one of the top three causes of opportunistic human infections. A major factor in its prominence as a pathogen is its intrinsic resistance to antibiotics and disinfectants. The authors now report the complete sequence of *P. aeruginosa* strain PA01. At 6.3 million base pairs, this is the largest bacterial genome sequenced, and the sequence provides insights into the basis of the versatility and intrinsic drug resistance of *P. aeruginosa*. Consistent with its larger genome size and environmental adaptability, *P. aeruginosa* contains the highest proportion of regulatory genes obsd. for a bacterial genome and a large no. of genes involved in the catabolism, transport and efflux of org. compds. as well as four potential chemotaxis systems. The size and complexity of the *P. aeruginosa* genome is proposed to reflect an evolutionary adaptation permitting it to thrive in diverse environments and resist the effects of a variety of antimicrobial substances. The genome and protein sequences are deposited in the GenBank database with Accession No. AE004091, as well at the web site <http://www.pseudomonas.com>.

IT 297290-35-8

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of *Pseudomonas aeruginosa* PA01)

RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 23 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1999:700747 CAPLUS
 DN 132:90427
 TI PhoP-PhoQ homologs in *Pseudomonas aeruginosa* regulate expression of the outer-membrane protein OprH and polymyxin B resistance
 AU Macfarlane, Emma L. A.; Kwasnicka, Agnieszka; Ochs, Martina M.; Hancock, Robert E. W.
 CS Department of Microbiology, University of British Columbia, Vancouver, BC, V6T 1Z3, Can.
 SO Molecular Microbiology (1999), 34(2), 305-316
 CODEN: MOMIEE; ISSN: 0950-382X
 PB Blackwell Science Ltd.
 DT Journal
 LA English
 AB Rapid adaptation to environmental challenge is essential for the survival of many bacterial species, and is often effectively mediated by two-component regulatory systems. Part of the adaptive response of *Pseudomonas aeruginosa* to Mg²⁺ starvation is over-expression of the outer-membrane protein OprH and increased resistance to the polycationic antibiotic polymyxin B. Two overlapping open reading frames that encoded proteins with high similarities to the PhoP-PhoQ two-component regulatory system of *Salmonella typhimurium* were identified downstream of the oprH gene. A *P. aeruginosa* PhoP-null mutant, H851, was constructed by means of a phoP::xylE-GmR transcriptional fusion, and shown to be deficient in OprH expression. In contrast, an analogous PhoQ-null mutant, H854 (phoQ::xylE-GmR), exhibited constitutive overexpression of OprH. Normal Mg²⁺-regulated OprH expression could be restored in both mutants by complementation with a plasmid carrying the phoP and phoQ genes. Measurement of the catechol-2,3-dioxygenase activity, expressed from the xylE transcriptional fusion in strains H851 and H854, indicated that PhoP-PhoQ is involved in the regulation of phoP-phoQ as well as oprH. Reverse transcription polymerase chain reaction expts. and Northern blot anal. revealed linkage of oprH, phoP and phoQ into an operon that was demonstrated to be under the joint control of PhoP-PhoQ and Mg²⁺ ion concn. In addn., studies of the polymyxin B resistance of the two mutant strains, H851 and H854, indicated that PhoP-PhoQ is involved in regulating *P. aeruginosa* polymyxin resistance in response to external Mg²⁺ concns.
 IT 254959-82-5
 RL: PRP (Properties)
 (amino acid sequence; PhoP-PhoQ homologs in *Pseudomonas aeruginosa* regulate expression of outer-membrane protein OprH and polymyxin B resistance)
 RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT
 L6 ANSWER 24 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1998:229920 CAPLUS
 DN 128:253667
 TI The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*
 AU Deckert, Gerard; Warren, Patrick V.; Gaasterland, Terry; Young, William G.; Lenox, Anna L.; Graham, David E.; Overbeek, Ross; Snead, Marjory A.; Keller, Martin; Aujay, Monette; Huber, Robert; Feldman, Robert A.; Short, Jay M.; Olsen, Gary J.; Swanson, Ronald V.
 CS Diversa Corporation, San Diego, CA, 92121, USA
 SO Nature (London) (1998), 392(6674), 353-358
 CODEN: NATUAS; ISSN: 0028-0836
 PB Macmillan Magazines
 DT Journal
 LA English
 AB *Aquifex aeolicus* was one of the earliest diverging, and is one of the most thermophilic, bacteria known. It can grow on hydrogen, oxygen, carbon dioxide, and mineral salts. The complex metabolic machinery needed for *A. aeolicus* to function as a chemolithoautotroph (an organism which uses an inorg. carbon source for biosynthesis and an inorg. chem. energy source) is encoded within a genome that is only one-third the size of the *Escherichia coli* genome. Metabolic flexibility seems to be reduced as a result of the limited genome size. The use of oxygen (albeit at very low

concns.) as an electron acceptor is allowed by the presence of a complex respiratory app. Although this organism grows at 95.degree.C, the extreme thermal limit of the Bacteria, only a few specific indications of thermophily are apparent from the genome. Here we describe the complete genome sequence of 1,551,335 base pairs of this evolutionarily and physiol. interesting organism. The 1512 open reading frames are classified into one of 3 categories, namely, identified, hypothetical, or unknown. A single extrachromosomal element (ECE) was also identified during sequencing. The sequences are available via GenBank Accession Nos. AE000657 and AE000667.

IT 204794-92-3

RL: PRP (Properties)

(amino acid sequence; the complete genome of the hyperthermophilic bacterium Aquifex aeolicus)

RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> s Lactococcus lactis

4379 LACTOCOCCUS

9417 LACTIS

L7 3817 LACTOCOCCUS LACTIS
(LACTOCOCCUS(W)LACTIS)

=> s l7 and casein

57367 CASEIN

22210 CASEINS

62902 CASEIN

(CASEIN OR CASEINS)

L8 234 L7 AND CASEIN

=> d his

(FILE 'HOME' ENTERED AT 13:57:27 ON 19 OCT 2004)

FILE 'REGISTRY' ENTERED AT 13:57:41 ON 19 OCT 2004

L1 25 S RDAKGE/SQSP

FILE 'CAPLUS' ENTERED AT 13:59:20 ON 19 OCT 2004

L2 25 S L1

L3 1 S L2 AND HYDROLY?

L4 2 S L2 AND ZINC

L5 1 S 388098-56-4/RN

L6 24 S L2 NOT L5

L7 3817 S LACTOCOCCUS LACTIS

L8 234 S L7 AND CASEIN

=> s l8 and hydrosy?

177 HYDROSY?

L9 0 L8 AND HYDROSY?

=> s l8 and hydrol?

602081 HYDROL?

L10 95 L8 AND HYDROL?

=> d ti 1-20

L10 ANSWER 1 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN

TI Continuous nisin production in laboratory media and whey permeate by immobilized *Lactococcus lactis*

L10 ANSWER 2 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN

TI Differentiation of intracellular peptidases of starter and adjunct cultures using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry

- L10 ANSWER 3 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN
 TI The obtaining of bioactive peptide material from products of proteolysis of .alpha.s- and .beta.-caseins
- L10 ANSWER 4 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN
 TI C-terminal end of .kappa.-casein is **hydrolysed** before renneting during soft cheese manufacture
- L10 ANSWER 5 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Synthetic peptides as substrate for assaying the proteolytic activity of *Lactobacillus helveticus*
- L10 ANSWER 6 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Malleable protein matrix and uses thereof
- L10 ANSWER 7 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Identification and characterization of *Lactobacillus helveticus* Pep02, an endopeptidase with post-proline specificity
- L10 ANSWER 8 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN
 TI The influence of starter and adjunct lactobacilli culture on the ripening of washed curd cheeses
- L10 ANSWER 9 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Applicability of a bacteriocin-producing *Enterococcus faecium* as a co-culture in Cheddar cheese manufacture
- L10 ANSWER 10 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Stabilization of cooked pasta compositions using whey from nisin-producing cultures
- L10 ANSWER 11 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Influence of growth conditions on the production of a nisin-like bacteriocin by *Lactococcus lactis* subsp. *lactis* A164 isolated from kimchi
- L10 ANSWER 12 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Changes in the microbiological and chemical characteristics of an artisanal, low-fat cheese made from raw ovine milk during ripening
- L10 ANSWER 13 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Immunoreactivity and inhibition of angiotensin I converting enzyme and lactococcal oligopeptidase by peptides from cheese
- L10 ANSWER 14 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Bacteriocin production by *Enterococcus faecium* FAIR-E 198 in view of its application as adjunct starter in Greek Feta cheese making
- L10 ANSWER 15 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Identification and characterization of lactic acid bacteria isolated from Tetilla cheese made from raw cow milk
- L10 ANSWER 16 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Cloning and expression of an oligopeptidase, Pep0, with novel specificity from *Lactobacillus rhamnosus* HN001 (DR20)
- L10 ANSWER 17 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN
 TI **Hydrolysis** of **caseins** and formation of hydrophilic and hydrophobic peptides by wild *Lactococcus lactis* strains isolated from raw ewes' milk cheese
- L10 ANSWER 18 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Debittering and **hydrolysis** of a tryptic **hydrolysate** of .beta.-casein with purified general and proline specific aminopeptidases from *Lactococcus lactis* ssp. *cremoris* AM2

L10 ANSWER 19 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN
TI Use of Fourier transform infrared spectroscopy to evaluate the proteolytic activity of Yarrowia lipolytica and its contribution to cheese ripening

L10 ANSWER 20 OF 95 CAPLUS COPYRIGHT 2004 ACS on STN
TI Utilization of amino acids and peptides and peptidase activities in proteinase- negative Lactococcus lactis FH 041

=> s l10 and zinc
533868 ZINC
95 ZINCS
533887 ZINC
(ZINC OR ZINCS)
L11 3 L10 AND ZINC

=> d ti 1-3

L11 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
TI Identification and characterization of Lactobacillus helveticus Pep02, an endopeptidase with post-proline specificity

L11 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
TI Composition comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics

L11 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
TI Purification and characterization of aminopeptidase P from Lactococcus lactis subsp. cremoris

=> d bib ab 2

L11 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:167822 CAPLUS
DN 134:206974
TI Composition comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics
IN Zlotkin, Stanley H.
PA Can.
SO PCT Int. Appl., 48 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2001015714	A1	20010308	WO 2000-CA990	20000828
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
CA 2281463	AA	20010226	CA 1999-2281463	19990826
PRAI CA 1999-2281463	A	19990826		
AB	A compn. useful for enhancing general immunity is disclosed. The compn. includes one or more micronutrients, one or more compds. selected from the group of a prebiotic, probiotic, and synbiotic, and lipid-based or carbohydrate-based excipient. Use of this compn. to enhance general immunity of the compn. is provided. A method of enhancing the general immunity of a mammal is provided, comprising the steps of removing a			

compn. comprising micro-encapsulated micronutrient granules, a substance selected from the group of a prebiotic, probiotic or synbiotic, and a pharmaceutically acceptable excipient selected from the group of a lipid-based excipient and a carbohydrate-based excipient from packaging material; adding a therapeutically effective amt. of said compn. to a food, and administering the food to said mammal.

RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d his

(FILE 'HOME' ENTERED AT 13:57:27 ON 19 OCT 2004)

FILE 'REGISTRY' ENTERED AT 13:57:41 ON 19 OCT 2004

L1 25 S RDAKGE/SQSP

FILE 'CAPLUS' ENTERED AT 13:59:20 ON 19 OCT 2004

L2 25 S L1
L3 1 S L2 AND HYDROLY?
L4 2 S L2 AND ZINC
L5 1 S 388098-56-4/RN
L6 24 S L2 NOT L5
L7 3817 S LACTOCOCCUS LACTIS
L8 234 S L7 AND CASEIN
L9 0 S L8 AND HYDROSY?
L10 95 S L8 AND HYDROL?
L11 3 S L10 AND ZINC

=> d ind 2

L11 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN

IC ICM A61K035-74

ICS A23L001-03; A23L001-303; A23L001-304

CC 17-6 (Food and Feed Chemistry)

Section cross-reference(s): 63

ST micronutrient prebiotic probiotic synbiotic food immunity

IT Gram-positive bacteria (Firmicutes)

(cocci; compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Bifidobacterium

Bifidobacterium adolescentis

Bifidobacterium animalis

Bifidobacterium bifidum

Bifidobacterium infantis

Bifidobacterium longum

Bifidobacterium thermophilum

Enterococcus faecium

Food additives

Food packaging materials

Immunity

Lactobacillus

Lactobacillus acidophilus

Lactobacillus brevis

Lactobacillus casei

Lactobacillus cellobiosus

Lactobacillus curvatus

Lactobacillus delbrueckii bulgaricus

Lactobacillus fermentum

Lactobacillus plantarum

Lactobacillus reuteri

Lactococcus lactis diacetylactis

Lactococcus lactis thermophilus

Streptococcus intermedius

(compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Fructooligosaccharides
 RL: FFD (Food or feed use); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Diglycerides
 Monoglycerides
 Waxes
 RL: PEP (Physical, engineering or chemical process); PROC (Process)
 (compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Monoglycerides
 RL: FFD (Food or feed use); PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
 (esters, of acetylated tartaric acid; compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Carbohydrates, biological studies
 Lipids, biological studies
 RL: FFD (Food or feed use); PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
 (excipients; compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Drugs
 (gastrointestinal, prebiotics; compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Bacteria (Eubacteria)
 (gastrointestinal; compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Oligosaccharides, biological studies
 RL: FFD (Food or feed use); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (gluco-; compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Coconut oil
 RL: FFD (Food or feed use); PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
 (hydrogenated; compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Soybean oil
 RL: PEP (Physical, engineering or chemical process); PROC (Process)
 (hydrogenated; compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Syrups (sweetening agents)
 (hydrolyzed starch, solids; compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Food
 (infant, additives; compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Anemia (disease)
 (iron-deficiency; compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Encapsulation
 (microencapsulation; compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Nutrients
 (micronutrients; compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Intestinal bacteria
 (probiotic; compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Caseins, biological studies
 RL: FFD (Food or feed use); PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process);

USES (Uses)
(sodium complexes; compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Drugs
(synbiotics; compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT Fats and Glyceridic oils, biological studies
RL: FFD (Food or feed use); PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process);
USES (Uses)
(vegetable, hydrogenated; compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT 7558-79-4, Dibasic sodium phosphate 7758-11-4, Dibasic potassium phosphate
RL: FFD (Food or feed use); PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process);
USES (Uses)
(compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT 57-48-7D, D-Fructose, oligomers, biological studies 127-47-9, Retinol acetate 141-01-5, Ferrous fumarate 585-86-4, Lactitol 4468-02-4, Zinc gluconate 4618-18-2, Lactulose 7439-89-6, Iron, biological studies 7440-66-6, Zinc, biological studies 7553-56-2, Iodine, biological studies 7720-78-7, Ferrous sulfate 9005-80-5, Inulin 11103-57-4, Provitamin A 15708-41-5, Ferric sodium EDTA
RL: FFD (Food or feed use); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

IT 9004-57-3, Ethyl cellulose
RL: PEP (Physical, engineering or chemical process); PROC (Process)
(compn. comprising micronutrients in combination with prebiotics, probiotics, and/or synbiotics)

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=> d que 15

L5 1 SEA FILE=CAPLUS ABB=ON PLU=ON 388098-56-4/RN

=> d ibib abs hitstr 15

L5 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:51115 CAPLUS

DOCUMENT NUMBER: 136:101570

TITLE: Method for preparing zinc-oligopeptide complex easily absorbable by the human body

INVENTOR(S): Sung, Kyu Ji

PATENT ASSIGNEE(S): S. Korea

SOURCE: Eur. Pat. Appl., 8 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1172373	A2	20020116	EP 2001-710010	20010306
EP 1172373	A3	20020410		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
US 2002028769	A1	20020307	US 2000-730542	20001207
US 6740502	B2	20040525		
JP 2002034592	A2	20020205	JP 2000-379180	20001213
CN 1333372	A	20020130	CN 2001-103060	20010122
CN 1392263	A	20030122	CN 2001-121932	20010620
CN 1392264	A	20030122	CN 2001-121933	20010620
US 2004126410	A1	20040701	US 2003-734172	20031215
PRIORITY APPLN. INFO.:			KR 2000-39595	A 20000711
			US 2000-730542	A3 20001207

AB Disclosed is a method for prepg. zinc-oligopeptides complex easily absorbable by the human body. A suspension of protein in deionized water at a neutral pH range in the presence of a protease is subjected to proteolysis to give a mixt. of oligopeptides. Zinc ions are chelated with the oligopeptides to give a zinc-oligopeptide soln. The zinc-oligopeptide soln. is concd. and dried to a powder. Also provided is a beverage or food compn. contg. the zinc-oligopeptide, which can make contribution to avoid the lack of dietary zinc. As an oligopeptide source, a vegetable protein such as bean protein and gluten, or an animal protein such as casein and gelatin was used.

IT 388098-56-4

RL: BUU (Biological use, unclassified); FFD (Food or feed use); BIOL

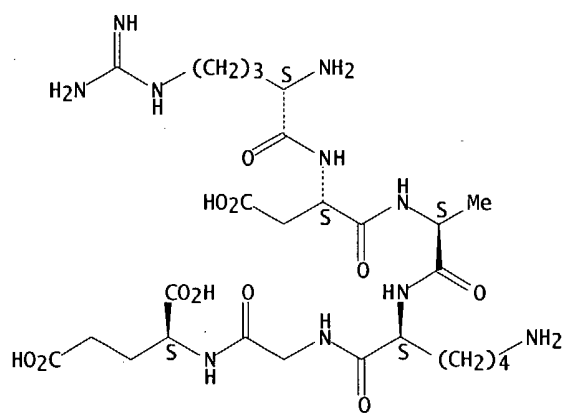
(Biological study); USES (Uses)

(method for prepg. zinc-oligopeptide complex easily absorbable by human body)

RN 388098-56-4 CAPLUS

CN L-Glutamic acid, L-arginyl-L-.alpha.-aspartyl-L-alanyl-L-lysylglycyl-(9CI) (CA INDEX NAME)

Absolute stereochemistry.



=>

=> s 388098-56-4

L12 1 388098-56-4
(388098-56-4/RN)

=> d all

L12 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2004 ACS on STN

RN 388098-56-4 REGISTRY

ED Entered STN: 30 Jan 2002

CN L-Glutamic acid, L-arginyl-L-.alpha.-aspartyl-L-alanyl-L-lysylglycyl-
(9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 6

SEQ 1 RDAKGE

SEQ3 1 Arg-Asp-Ala-Lys-Gly-Glu

MF C26 H46 N10 O11

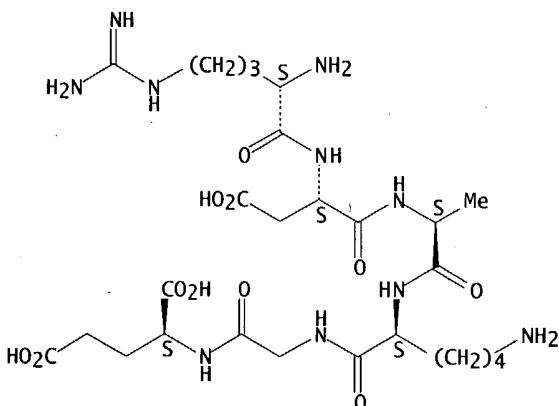
SR CA

LC STN Files: CA, CAPLUS, USPAT2, USPATFULL

DT.CA CAPLUS document type: Patent

RL.P Roles from patents: BIOL (Biological study); USES (Uses)

Absolute stereochemistry.



Calculated Properties (CALC)

PROPERTY (CODE)	VALUE	CONDITION	NOTE
Freely Rotatable Bonds (FRB)	36		(1) ACD
H acceptors (HAC)	21		(1) ACD
H donors (HD)	16		(1) ACD
logP (LOGP)	-5.499+/-1.059		(1) ACD
Molecular Weight (MW)	674.70		(1) ACD
pKa (PKA)	3.45+/-0.10	Most Acidic	(1) ACD
pKa (PKA)	13.46+/-0.36	Most Basic	(1) ACD

(1) Calculated using Advanced Chemistry Development (ACD/Labs) Software
Solaris V4.76 ((C) 1994-2004 ACD/Labs)

See HELP PROPERTIES for information about property data sources in REGISTRY.
 1 REFERENCES IN FILE CA (1907 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1

AN 136:101570 CA
 TI Method for preparing zinc-oligopeptide complex easily absorbable by the human body
 IN Sung, Kyu Ji
 PA S. Korea
 SO Eur. Pat. Appl., 8 pp.
 CODEN: EPXXDW
 DT Patent
 LA English
 IC C07K007-06; C07K014-415; C07K014-435; A23L001-304; A23J003-34
 CC 17-13 (Food and Feed Chemistry)
 Section cross-reference(s): 13

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 1172373	A2	20020116	EP 2001-710010	20010306
	EP 1172373	A3	20020410		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	US 2002028769	A1	20020307	US 2000-730542	20001207
	US 6740502	B2	20040525		
	JP 2002034592	A2	20020205	JP 2000-379180	20001213
	CN 1333372	A	20020130	CN 2001-103060	20010122
	CN 1392263	A	20030122	CN 2001-121932	20010620
	CN 1392264	A	20030122	CN 2001-121933	20010620
	US 2004126410	A1	20040701	US 2003-734172	20031215
PRAI	KR 2000-39595		20000711		
	US 2000-730542		20001207		
AB	Disclosed is a method for prepg. zinc-oligopeptides complex easily absorbable by the human body. A suspension of protein in deionized water at a neutral pH range in the presence of a protease is subjected to proteolysis to give a mixt. of oligopeptides. Zinc ions are chelated with the oligopeptides to give a zinc-oligopeptide soln. The zinc-oligopeptide soln. is concd. and dried to a powder. Also provided is a beverage or food compn. contg. the zinc-oligopeptide, which can make contribution to avoid the lack of dietary zinc. As an oligopeptide source, a vegetable protein such as bean protein and gluten, or an animal protein such as casein and gelatin was used.				
ST	zinc oligopeptide complex prepn absorption body				
IT	Drug delivery systems (capsules; method for prepg. zinc-oligopeptide complex easily absorbable by human body)				
IT	Protein degradation (for oligopeptide prepn.; method for prepg. zinc-oligopeptide complex easily absorbable by human body)				
IT	Drying (for powder prepn.; method for prepg. zinc-oligopeptide complex easily absorbable by human body)				
IT	Beverages (method for prepg. zinc-oligopeptide complex easily absorbable by human body)				
IT	Proteins RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses) (method for prepg. zinc-oligopeptide complex easily absorbable by human body)				
IT	Concentration (process) (of zinc-oligopeptide complex, for prepn.; method for prepg. zinc-oligopeptide complex easily absorbable by human body)				

IT Caseins, biological studies
 Gelatins, biological studies
 Glutens
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
 (oligopeptide source; method for prepg. zinc-oligopeptide complex easily absorbable by human body)

IT Peptides, biological studies
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
 (oligopeptides; method for prepg. zinc-oligopeptide complex easily absorbable by human body)

IT Drug delivery systems
 (powders; method for prepg. zinc-oligopeptide complex easily absorbable by human body)

IT Diet
 (supplements; method for prepg. zinc-oligopeptide complex easily absorbable by human body)

IT Drug delivery systems
 (tablets; method for prepg. zinc-oligopeptide complex easily absorbable by human body)

IT 9000-90-2, .alpha.-Amylase
 RL: FFD (Food or feed use); BIOL (Biological study); USES (Uses)
 (decompd. starch; method for prepg. zinc-oligopeptide complex easily absorbable by human body)

IT 7732-18-5, Water, biological studies
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
 (deionized; method for prepg. zinc-oligopeptide complex easily absorbable by human body)

IT 7440-66-6, Zinc, biological studies
 RL: BCP (Biochemical process); FFD (Food or feed use); BIOL (Biological study); PROC (Process); USES (Uses)
 (method for prepg. zinc-oligopeptide complex easily absorbable by human body)

IT 9001-92-7, Proteinase
 RL: BUU (Biological use, unclassified); CAT (Catalyst use); BIOL (Biological study); USES (Uses)
 (method for prepg. zinc-oligopeptide complex easily absorbable by human body)

IT 388098-56-4
 RL: BUU (Biological use, unclassified); FFD (Food or feed use); BIOL (Biological study); USES (Uses)
 (method for prepg. zinc-oligopeptide complex easily absorbable by human body)

IT 50-81-7, Vitamin-C, biological studies 57-48-7, D-Fructose, biological studies 59-43-8, Vitamin-B1, biological studies 83-88-5, Vitamin-B2, biological studies 557-04-0, Magnesium stearate
 RL: FFD (Food or feed use); BIOL (Biological study); USES (Uses)
 (method for prepg. zinc-oligopeptide complex easily absorbable by human body)

IT 9005-25-8, Starch, biological studies
 RL: FFD (Food or feed use); BIOL (Biological study); USES (Uses)
 (.alpha.-amylase decompd.; method for prepg. zinc-oligopeptide complex easily absorbable by human body)

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